

Query No.	Score	Match length	DB	ID	Description
c 1	1416	95.9	172832	8	AL358412
c 2	1416	95.9	173352	10	AL358412
c 3	1416	95.9	173761	11	AL358412
c 4	1416	95.9	173768	9	AL358412
c 5	1416	95.9	178044	12	AL358412
c 6	1416	95.7	179542	13	AL358412
c 7	1404.8	95.2	179698	16	AL358412
c 8	1404.8	95.2	179700	15	AL358412
c 9	1404.8	95.2	179700	15	AL358412
c 10	1383.2	93.6	170967	17	AL358412
c 11	1133.8	76.7	121645	5	AL358412
c 12	1084.4	73.5	161974	3	AL358412
c 13	1084.4	73.5	161974	4	AL358412
c 14	1084.4	73.5	161974	4	AL358412
c 15	1009.2	68.4	172266	6	AL358412

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C	36	45.2	001	3.1	9462	18	AL358412	ACCESSION:AL358412

ALIGNMENTS

[illegible]

On Nov 1, 2000 this sequence version replaced gi:11043617.

Center: Sanger Centre

Center code: SC

Web site: <http://www.>

Contact: humquerry@sat.fr

----- Project

Center project name: Summary

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----- Summary -----
Assembly program: XGA
```

Assembly: AGH
Sequencing vector: pJ

Chemistry: Dye-terminating

Consensus quality: 16

Consensus quality: 16

Consensus quality: 16

Insert size: 171322;

Invert size: 189168;

Quality coverage: 5.00

coverage: 4.73x in Q2

* NOTE: This is a two

* NOTE: THIS IS A TWO
* PAGE SET OF 16 CONT

* COLIBSLS OF 16 CONT
* is not known and th

* arbitrary. Gaps bet

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* This record will be

★ as soon as it is av

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                  154140..172822
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                  fragment_chain:4
                  clone_end:SP6
                  vector_side:right"

Query Match      95.9% ; Score 1416; DB 8; Length 172822;
Best Local Similarity 4.9%; Pred. No. 2.5e-08;
Matches 1476; Conservative 0; Mismatches 0; Indels 28706; Gaps 6

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[illegible]

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QY 181 ----- 180
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QY 181 ----- 180
Db 24205 GACTCATATCACTTGTATGTGATCTTCTTTTCTGTGTCAGATTTGCTTTTGGGC 24146
QY 181 ----- 180
Db 24145 ACAGAGACTCACACTAATATTCAAAGACTTGTGAGCATATGAGAGATCGCTTGA 24086
QY 181 ----- 180
Db 24085 GCCCCAAGAGTTGAGACCAAGCCTGGGCACAATGTGAGGCCCTGTCAAAATTAAGAAA 24026
QY 181 ----- 180
Db 24025 AAGAGAGAAATACGTCTTTTCTTTTCAATGCTTTTATCTGTATCTATCTACTAT 23966
QY 181 ----- 180
Db 23965 TCTGCTCTAATAAGAAATAGTTCACTCTTGAGTTTATAAAAACGTATGCTTCAT 23906
QY 181 ----- 180
Db 23905 GTGTGATTTATTAACAATCTTATTTGTAACTTTCTCTGTGTTACATTTATTTTCTG 23846
QY 181 ----- 180

Db 23845 AAACCTAGTCTGCTTTAGCTGACATGTGTGTAGCTAAGAGCGCACATTTCTATACATA 23786
QY 181 ----- 180
Db 23785 GCTTGCCGTGTAATTAATTCATTTTCTTTAAAAACAATATATGATTAATG 23726
QY 181 ----- 180
Db 23725 TATAAGAAATAACTGTTCCTCATTTTAAAGTATACAAATTGATGATTTTGACAAAAGTG 23666
QY 181 ----- 180
Db 23665 GGACCCACGTAACCAACCAACAATCAAGATGTAGACGTTCTATACACCCAGAAAAG 23606
QY 181 ----- 180
Db 23605 TTCCCTGATCCACTTTGATTCAGGCTTCAGATCTAGGCAACCAAGATCTGTTCTG 23546
QY 181 ----- 180
Db 23545 ACACTGTGATTAACCTTGCCTGTTCAGATTTTCATATAAATGATGTATAGTATG 23486
QY 181 ----- 180
Db 23485 TACCTTTGCTGTGCTGCTCTTCCCTCAGCATATATGTTCTGAAAATTCACCCACATG 23426
QY 181 ----- 180
Db 23425 TTACATGATACGATAGTAAATTCCTTTTATTTGTGTAGTATGCAATGCAATGATGACTA 23366
QY 181 ----- 180
Db 23365 TGTATGACATTTGTTAATCCATTTTCCCTGATGATATTTGGGTGCTTCCAGTTCTG 23306
QY 181 ----- 180
Db 23305 GGACGATATCATTTGCTAGGGCTGCCATATGCTTGCCCTGTGGCCTCCCAAAATTTGTG 23246
QY 181 ----- 180
Db 23245 TCTTTTCATATGCAAAATACATTAACCCCTCCCAAGCCCCCAAACTCTCTTTT 23186
QY 181 ----- 180
Db 23185 TTTTGTGAAAAGAGTTTGTCTGTGTGCCAAGCTGAGTGCATGTGTATCT 23126
QY 181 ----- 180
Db 23125 CGGCTACGCAACCTGCTCCGGGTTCAAGAGATTCCTGCTCAGCCTCGTAG 23066
QY 181 ----- 180
Db 23065 TAGCTGGATTACAGGATGCGCAACAGCCTGGCTAATTTTATATTTTATAGTAA 23006
QY 181 ----- 180
Db 23005 ATGGGGTTTACCGGTATGACAGGCTGTGAACTCTGACCTCAAGGTATCGGCT 22946
QY 181 ----- 180
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QY 181 ----- 180
Db 22885 AAACCTTAACCATTTCAAGATCTACTTAAGTCCAAAGTCTCATTAATCAGGTATG 22826
QY 181 ----- 180
Db 22825 GGTGTACTGAGGTGTACTCATCTCGAGGCCAAATTCCTCTCCACTATGAACTGTG 22766
QY 181 ----- 180

Db 22765 AACACGACAGGTTATGTGCTTTGAAAAATAAAGTATGGGACATGCATGGGATAGACTTT 22706
QY 181 ----- 180
Db 22705 CCCATTCGAAAAGAAAAATAGAGAAAGAGAGAGACAGTCCGACAGCAAGTCTA 22646
QY 181 ----- 180
Db 22645 AAACCTGCAAGGCAAAATTCATTAGATTTTAAGTTTCAAGAAATAGCCCTCTTTGGCTCA 22586
QY 181 ----- 180
Db 22585 GTGCTGCCCCCTTGGGGCCACTGGGGCGGAGCCCTATCCCTTGGCCCTGGGTGTGA 22526
QY 181 ----- 180
Db 22525 CCCATCCCTGAGTCACTGGTTAGACAGAGCTAGCCTGCTGAAACTTAAGAGGGAGACAG 22466
QY 181 ----- 180
Db 22465 TGTTGCTCCAGGTCTTTGGTGGCAGTGAACCCCTGATCTGMAATCATCTTCCAG 22406
QY 181 ----- 180
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QY 181 ----- 180
Db 22345 GTCCCTTCTTTAGATATCCAGAAAGTCCAAAGCCCTTCTTCATCTGTCCCATCTCTGT 22286
QY 181 ----- 180
Db 22285 CCCCTTAGTCAAGGTGAGAGTCTCTGCTGTATATATCCCATGATATGCTAATTT 22226
QY 181 ----- 180
Db 22225 CTGCTTAATAGGCTAATTAAGTATAGTATAGTTGCAACCCTGATCTCTTATCAAAAGTTG 22166
QY 181 ----- 180
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QY 181 ----- 180
Db 22105 GTGATAGGCTGAAATTTTCCAAAGCTTGAATTCATGTTCTTTGGCTTACCAATTC 22046
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QY 181 ----- 180
Db 21985 CTTCAGACCTTGGCTTAGAAATCTCTTCTGCTAAGCATCCAGTTTATGTCTTTTAAT 21926
QY 181 ----- 180
Db 21925 ATCTTTTGTATTATTTATATATATATCAATTTTGAATGGCTAGCCAAATGAATTTTA 21866
QY 181 ----- 180
Db 21865 CTTCATATTTCTGCAAAAACCTAGAAAGACATTCAAACAGTCTTGGCCATTTATACAA 21806
QY 181 ----- 180
Db 21805 AGGATCACCTTCTCCAGTTTCCAAATACACATTCCTTTTCCACGTAGACCTCAAC 21746
QY 181 ----- 180
Db 21745 AGAATCACTTATATGTCTATATTTCTACCAATAGTCTTTTAAAGCAATATAGGCTTTC 21686
QY 181 ----- 180
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QY 181 ----- 180
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QY 181 ----- 180
Db 21565 GCTAGGCTGCCATACAAAGTAGACAGTCTGGGTAAACAAGAAATTTTATTTCTCA 21506
QY 181 ----- 180
Db 21505 AAATTCAGAGTTGGAATGCCAAGTCCAAAGCGTGTAGTTAGTTTCTCCTGAAGC 21446
QY 181 ----- 180
Db 21445 CTCTCTCTGGCTAGCAGATGGCTGCTTCTGTGTCTTCAAGCTTTTCTCT 21386
QY 181 ----- 180
Db 21385 GTGTGTTCACCTGTGATCTCTTCTCTTACAAAGTACACCAAGCTACTGATTA 21326
QY 181 ----- 180
Db 21325 GGGCCGAGCCTTATTACTTATTTAACATTAATTAACCTTTAAAGCTTATCTCAAA 21266
QY 181 ----- 180
Db 21265 ACACATACACATGGGATGAGTCTTCACATATGAATTTTGGGGAACTCAATTCGTC 21206
QY 181 ----- 180
Db 21205 CATATAGGCTATATGAAATTAAGCTGTGTGAACATTCATGCAAGTCTTGTGTGG 21146
QY 181 ----- 180
Db 21145 ATATGTTTCAATTTCTCTAGATAAAGTCTAGAGATATCAGCCTGGGCAATATGTAG 21086
QY 181 ----- 180
Db 21085 AACCCTTTTACAAAATTTTCAAAATTAAGCCAGCATGTGGCGTACACTGTAGCC 21026
QY 181 ----- 180
Db 21025 CTGCCATCTAGAGGCTGAGGTGGAGAGATCCCTTAGCCGAGGGTTTAACTGAC 20966
QY 181 ----- 180
Db 20965 TGAATGATTGACACACTGCAACCCAGCCTGGGTGACAGATGAGACTCTGTCTTAA 20906
QY 181 ----- 180
Db 20905 AAAAAAGAGAGAGGGGAGAGAGAAAAGAAAGAGAGAGGAGGAGAGGAG 20846
QY 181 ----- 180
Db 20845 GGAGGAGAGAAAAATGATCTAGGGTTAAGATTAGATTAAGATTAAGATAATGTGTA 20786
QY 181 ----- 180
Db 20785 CTATTAAGGGAAGTGTGAGCTGTTTCCAAAGTACTGATCAATTTGATTTGCCACCA 20726
QY 181 ----- 180
Db 20725 ACAATACATAGAGTTCTAGTACTCATGTGCTGTATCACTTAGATATACAGTCTT 20666
QY 181 ----- 180
Db 20665 TTCAATTTAACCATTTAGTAGAGTAGTAGATTTATATATGCTTTAATTACAAAC 20606
QY 181 ----- 180
Db 20605 TCCCTAATGATGATGATGTTGAACATCTTTTCATGAGCTTATTTGGCATTCATATATCT 20546

QY 181 ----- 180
Db 20545 TTGTGAGTACTATTCAAATATTTTCCACTTTTATAGTCATTTATTTCTTATT 20486
QY 181 ----- 180
Db 20485 ATTGAGTATCTATGAATACAAATCCCTTTATCAGTGATGTATTTGATTTTCCCA 20426
QY 181 ----- 180
Db 20425 GTGGCTGCCCTTTCATTTGCTTAGGCTTTTGTGGGTTTTTTTTTTTGGAA 20366
QY 181 ----- 180
Db 20365 GAGAAAAATATTTAATTGATTAATAATCCAGTATATCAGGTGTATAGACTGAATTATAC 20306
QY 181 ----- 180
Db 20305 TCTACCCCAAAATTCATATGTGAGCCCTAACCTTAAGTACTATTTGGAGATGAGC 20246
QY 181 ----- 180
Db 20245 CTTTAAGGAGGTAATTAAGTAATGAGATCATTAAGGTGGGCCCTAATCTAATAGAC 20186
QY 181 ----- 180
Db 20185 TGGTGCTTTTATAGAGAGAGACACCAAGAGCCGATGACACACAGAAAGCGCCTTG 20126
QY 181 ----- 180
Db 20125 TGAGACACAGCAGATGAGGCGCATCTGCAAGCCAGAGAGAGCCTCAGTAGAAACC 20066
QY 181 ----- 180
Db 20065 AAACCTGTGATGCTGTGATCTTGAGACTTCAGCCTCCAGATTTCTGTGCTGAGCCAC 20006
QY 181 ----- 180
Db 20005 CCTGCTGTGGTGTCTTACCATGCGACGCTCACAGACTAATATACAGATTTTTTCT 19946
QY 181 ----- 180
Db 19945 TCACAGATTAACGCTTTTGGTGTCTTACGAAATATTTGGCCTGACCCAGGCTCATGAGAT 19886
QY 181 ----- 180
Db 19885 TTTTCTTCTAAGCTTCTCTGSAAGTCTATAATTTAGCTTTTACATATTTTTTAAAC 19826
QY 181 ----- 180
Db 19825 TTTCCTTCTTCTGCTTCTGCTTCTTTAAGGCATCATATGTGTAATTTGTTCT 19766
QY 181 ----- 180
Db 19765 GATATCTCTGTATTAATCTTCACTTCTGAATGAATTTTGCTTTTAAATATATAT 19706
QY 181 ----- 180
Db 19705 AATCTTTTCTGTCTGAGTTTCTAAATAGGTTTATAGGTTTTTCTGTGCTGTC 19646
QY 181 ----- 180
Db 19645 ATCACTTTTACTGTCTTTTGGCCATTTTGAAGTATCAGAGTTCAGCTTTGATCTGTTCA 19586
QY 181 ----- 180
Db 19585 TGAATATGTTTTTGACAGATTTCTTGGCTTCTTATCATTATATGCTTAGCTTAATA 19526
QY 181 ----- 180
Db 19525 ATTTCATTTCTTTCTATTTTCTATTAATTAAGTATTAAGCTATATGTTTTCTCTAAGT 19466
QY 181 ----- 180

Db 19465 ATTACTTAGCTGTCTATTAACGTTTTCAATTTGHTAATTTGGNGATCATTTCACTTGACGT 19406
QY 181 ----- 180
Db 19405 ATTTATTAATTTCCATTATTAATTTCTTCATCTAGGTGTGTTTTAAAAATATTTTTAAG 19346
QY 181 ----- 180
Db 19345 GCCAGGTGTGACTCAATCTGTATCAGACACTTAGGAGGCTGAGGTGGAGGAT 19286
QY 181 ----- 180
Db 19285 TGCTTAGGCCAGAAATTGAGACCGGCTTAGCAACAAGTAGACCCCTCTCTACAG 19226
QY 181 ----- 180
Db 19225 AATATTTTTTAAATTAGCTGGGCCAGAGGTGTGCTCATCCAGCACTGTATATACC 19166
QY 181 ----- 180
Db 19165 AGCACTTTGGAGGCCAAGCAGATGATCATCTGAGGTGAGAGTTGAGACAGCCTG 19106
QY 181 ----- 180
Db 19105 GGCAACATGTAAACCCCATCTTTACTAAATATMAAAATTAGCCAGGTGTGTATAG 19046
QY 181 ----- 180
Db 19045 GTGCTGTAAATCCAGCTAATTGGGAGGCTGAGGAGAGAAATTTTGAACCCAGAGG 18986
QY 181 ----- 180
Db 18985 AGGAGTTGACGTAGACCGAGATTGCACACTGCACCTCGATGACAGAGCGAGA 18926
QY 181 ----- 180
Db 18925 CTCTGTCAAAAAAAGAAAAAAGAAATTTAGCTGGGTGTAGTGGCAGTACTGTGG 18866
QY 181 ----- 180
Db 18865 TCCAGTACTCAGAGCTGAGGAGAGATCACTGAGCCGAGATGAGGCTGAG 18806
QY 181 ----- 180
Db 18805 TGAAGTATGTTTGCCACTGCACTCCAGCCTGTGCAACAGAGCAAGCGCTGTCTAAA 18746
QY 181 ----- 180
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QY 181 ----- 180
Db 18685 AACTGAATGTTTGCAATCAGAGAAATCTTTATAGATACCTATCTTTAAAAATTTCT 18626
QY 181 ----- 180
Db 18625 TAAGAAATGCTTTGTGTAATATTTTGTAAATAGTGCAGATGCGTTCAACCAATTTGT 18566
QY 181 ----- 180
Db 18565 TAGTTAGTCTGTATATATGTTCAATTAGCACACTTGATTAAGTGTGTTCTTATTTATT 18506
QY 181 ----- 180
Db 18505 TATGTATTAATTTTCTTTGCTATTCATCATCAATGTGCGGTGAGATGTATTAATTTCT 18446
QY 181 ----- 180
Db 18445 TGTTGTAAGTGTGCGGTCACTTTCTACCTGTAGTTTGTGTGCTTTATAGAGGGT 18386
QY 181 ----- 180

Db	18385	GAAAGTGGTTTAGTAGGCAACATAAGTTAGATTTTCTCTCTTCTGCTGGAATGGAATC	18328
OY	181	-----	180
Db	18335	ATTATCATATCTAATAGTCTTTTCATCTTAGTATGCTTTGGAATTGAACTGTGA	18266
OY	181	-----	180
Db	18285	TTTGTCTCTGTTAATATACTACACTGGTCTTGGTGAAATTTGGCATAGTATA	18206
OY	181	-----	180
Db	18205	ACATTTTCATGGAAGAAACAAACAGAGAAATGGTCTTCTCAAAATCTGATCTTTGT	18146
OY	181	-----	180
Db	18145	GTCAGCCCCCATCTCAGCCTTCTCCATTCACTTGGTCACTCCCAACCAAGAGCA	18086
OY	181	-----	180
Db	18085	TCCTTGATTCCTTTTCCCACTTCTACATCCATCCGTAGCAAGTTCTATTACTTC	18026
OY	181	-----	180
Db	18025	TATTATTACCTCCAAATAGATATGAATCAGCCCTTCTCAGCTCTCCACCATATC	17966
OY	181	-----	180
Db	17965	CTGCTCACATCCCTACCATAGCCTCCTCTGCTGTTGACCAGAGATCTGTAAAAACA	17906
OY	181	-----	180
Db	17905	TGTTAGCCACAGCACGCTGGCTCCTGCTGTAACTCCAACTTTGGAGGCCAAGCGGG	17846
OY	181	-----	180
Db	17845	TGGGTCACTGAGGTCAAGAGTTGAGACCAAGCTGAGCCAGATGATGAACCTGTCTC	17786
OY	181	-----	180
Db	17785	TACTAAAAATACAAAAATTAGCCAGGTGTGTAGCGTGGCTGTATATCCATCTACTGG	17726
OY	181	-----	180
Db	17725	GAGGCTGAGCAGAGAGATCACTTGAAACCCAGAGAGCGAGGTTGACGTGAGCCAAGATC	17666
OY	181	-----	180
Db	17665	ATGCCACTGCACCCACGCTGGGCAACAGAAAGACTCCATCTCAAAAAATAAAAATTA	17606
OY	181	-----	180
Db	17605	AAATAAATGTTAGGCTCCCTGGGCTCTGGCTTACTGCATTGTACTGTTAACAAA	17546
OY	181	-----	180
Db	17545	TACCTTAGAATGGGTATATTCTATATATTCGTATTATATAATATAGCAATTATATAATA	17486
OY	181	-----	180
Db	17485	ATAGCAATTTCTTCTACAGATCTTAGAGGCTGGAGAAATTCAAGGTCAAAGTGGCACTCG	17426
OY	181	-----	180
Db	17425	ACTCCGTTCTGTAAAGGCGGCTCTCTGCTTCCAAAGATGGTCCCTTCTGCTCGCTCTTC	17366
OY	181	-----	180
Db	17365	GCATAGCGAAGGCAAAACACTGTGTCTCACTGAGCAAGAGATAGAGGCGCAAGCA	17306
OY	181	-----	180
Db	17305	GCTCTCTGAATATATCAAGGTTGAGTGCATGACCTGCATGTTCCCTCTGCATCCACAG	17246

QY	181	-----	180
Db	17245	AGTACTTATCATGGTCTTGGCATGCACAGGTGGCCCATTAACGCTGAATGACAAAC	17188
QY	181	-----	180
Db	17185	ATATAGTAATGATGCTAGTACTAGAAATAGCAGCCACGCAACAAGTGTGAGGAGG	17120
QY	181	-----	180
Db	17125	CATTACAGATAGGAAACTGAGGTTTAGGGCAAAGACTGGCCATGATGCCAAAGCTAG	17066
QY	181	-----	180
Db	17065	GAGGGACAGGGCTGGGATTCCGACTCCATCCATCTGGCTCCAGAACTGATCCTGA	17006
QY	181	-----	180
Db	17005	CCAGGCTGTTCTTCTCTGTTCTACGCCATGGCTGCTGTGACGATGACCTTAAG	16946
QY	181	-----	180
Db	16945	TCACTCCAGCCAAACAGAGGAAAGCATGATCACTGTTCTTAAGTTCCTGACCCGGAG	16886
QY	181	-----AGCTTCCCAACCGGTGAGG	200
Db	16885	AGGCTGATGTCATGAGCCCAAGCTCTCTCTCTCCCCAGGCTTCCCAACCGTGAAG	16822
QY	201	GTGGCGGAAATGGAAGATGTGCGGAAACCAAGAGCTGTATGTTCTATGATGCT	260
Db	16825	GTGCGGGAATGTGAAGATGTGCGGAAACCAAGAGCTGTATGATGATGCT	16766
QY	261	GAAAGAACGAGACCTGTACAAACAAGTTCAAGGGAACGCGTGGCGGACGGTTTCCAGACTC	320
Db	16765	GAAAGAACGAGACCTGTACAAACAAGTTCAAGGGAACGCGTGGCGGACGGTTTCCAGACTC	16706
QY	321	CAAGTCCCCCTGGGTGAGTCCGAATACCTGATTAACCTTTTGA	365
Db	16705	CAAGTCCCCCTGGGTGAGTCCGAATACCTGATTAACCTTTTGAAGGTGCTGTGGG	16646
QY	366	-----	365
Db	16645	TAAAGGACTAGTGAAGGCTGTCCATCCATCGGGAGCTGTCTCACTGCTCACTGGT	16586
QY	366	-----	365
Db	16585	TCTGTCTCCTGACCAATCTGTCTCCCACTTCCCAAGACAGAGGAGCTCCCTGGGCA	16526
QY	366	-----	365
Db	16525	GGCCCTTGAAGATGGGCTGTGGACCAAGCAACGCGAGGACCAATGTCTGGACGCTGTC	16466
QY	366	-----	365
Db	16465	AGGAGTTAAGGAGCTCCAGCCAGACCAAGCAATCTCACTGACACCTCTGCTAAAT	16406
QY	366	-----	365
Db	16405	GTTTCATTATTTTCAAGTTGAGCACCAATTTGTTCATGACTACACAAGGCACTTTATATGC	16346
QY	366	-----	365
Db	16345	TTATTCCTATTTTATATGTTCAGCTTCTCTCTAATAAACAATGTTTAAACCAATCTG	16286
QY	366	-----	365
Db	16285	GAGCAGGCGTGTGGCTCAAGCCTGTAAATCCAGCACTTTGGGAGGCCAAGCAGGTGA	16226
QY	366	-----	365
Db	16225	TCACTGAGGCTCAGAGTTTGAACCAACCTTGAGCAATGCGCAAAACCCGCTTTACT	16166

[illegible]

Db	15085	GTGGCCCTGTAGTCCCACTGCTGTGGGAGGCTAAGCAGAGAGATGGCGTGAACCCAGGA	15026
OY	366	-----	365
Db	15025	GGCAGAGCTTGCACTGAGCTGATGCTGTCACCTGACCTTGCAGCTGGGTGACAGACAA	14966
OY	366	-----	365
Db	14965	GACTCCCTCTCAAAATAAATTAATTAATAATAATAAAGGCCAGCCATGTGGCTCACA	14906
OY	366	-----	365
Db	14905	CCTGTAACTGAGCACTTTGGAGGCCGAGCGGATGATCTTTGAGATCAGAGATTCA	14846
OY	366	-----	365
Db	14845	AGACCAGCCTGGCCACAATGCTGAAACCTGTCTCTTAATAAAATTAATAAAGTTACCGGT	14786
OY	366	-----	365
Db	14785	GTGTGTGGCAGACAGACCTGTAGTCCAGACTACAGAGAGCTGAGGCAAGAAATGCTT	14726
OY	366	-----	365
Db	14725	GAACTTGGGAAGCAGAGGTTGCAGTGAAGCTGAGATACGACACTGCACTCCAGCTGGGT	14666
OY	366	-----	365
Db	14665	GACAGAGCAACTTGTCTCAAAAAAAAAAATTTAATAAGAAGAAATTAATTATGG	14606
OY	366	-----	365
Db	14605	GAATTTGGCTATGCAATCAGACACAAAAATGTCCCCAGATCACTCATGGGCTGGA	14546
OY	366	-----	365
Db	14545	CAACAGAGAAAGCTTGTGTGTGATTTCTGTGAGCTGAAAGCCCAAGCCAGGGAGGC	14486
OY	366	-----	365
Db	14485	AGTGTGTAAACCCAGTCGGAGGCCACAGGCCAACATCAGAGGGGCCACTGATATTA	14426
OY	366	-----	365
Db	14425	GTCCAGAGTCCAAATGCCGAGAACAGAGAGCTCCAAATGCCAAGACAGAGAAAGTTG	14366
OY	366	-----	365
Db	14365	ATGTGCCAGCTCAGAGAAAGAGAAATGTGAATGTGCATTTCTCTCCATTTTTTGTCTC	14306
OY	366	-----	365
Db	14305	TTTGGGCCCTCAGTGGATTGATGATGCTGTCCCACTGTGTGAGACAGATCATCACCA	14246
OY	366	-----	365
Db	14245	AATCTGCCAATTAATGTATATCTTCTGTGAAAAATCTCAAGATGGGCCAGAAAT	14186
OY	366	-----	365
Db	14185	AATGTTTACTGTCTACCTGGGTATCCCTAGTGACGTAATTGACATATAACTTAAC	14126
OY	366	-----	365
Db	14125	CATCAGAGGACAGCACTGTGGCTCACACCTGTATCCATCACTTTGGAGGCCAAGGT	14066
OY	366	-----	365
Db	14065	GGGAAATCTTTGAGATGAGGTAGAGCAATCACTGAAGCTTAGAGATTCAAGACACGC	14006
OY	366	-----	365

Db 14005 CTAAGCAACATAGGAGACCTCGTCTACAAAAAATAATTAAATCGCTGGGT 13946
QY 366 ----- 365
Db 13945 ACGGTGGTGGGCACTGTGTGTCCAGCTATCTGGAGGCCAAGTAGAGATGACTTGA 13886
QY 366 ----- 365
Db 13885 GCCCAGAGGTCAAGGCTGCAGTAGGCCATGATTGTTCCATTGAATTCAGCCTCGGTGA 13826
QY 366 ----- 365
Db 13825 CAGAGCAACACCTGTCTTTAAGAAAAAATTTAACCATCACAGAGCCAGAAAGAA 13766
QY 366 ----- 365
Db 13765 AGGCAGATGGGTGATGATGATGGGTGATAGTATAGAAAAAGCAAGACATCCAG 13706
QY 366 ----- 365
Db 13705 GCAAGGAAAGGAGGCTGAGCGAAGAGAAAGAAAGAAAGAAAGAGAGAAAGAA 13646
QY 366 ----- 365
Db 13645 GAAAGATGTGTAGAAAGGTGAAAGAAAAAGAAATGATGTATGGAAAGAAATGGATG 13586
QY 366 ----- 365
Db 13585 AGTAGTTAGAAAGCTCATGCTGTAGATAAAGGTGAAAGTAAATGATATATAGAA 13526
QY 366 ----- 365
Db 13525 AGGAGCATAGGAAAGAAAAAATTTGGTTAGAAAAGATGATTGAGAAAGAGGTGTT 13466
QY 366 ----- 365
Db 13465 GGGAAAGAAAGAAAGAAAGATGATGATGATGATGATGATGATGATGATGATGATG 13406
QY 366 ----- 365
Db 13405 GATTAAGAAAGCAAGCAGAGAGGCTCTGTGGCTAGAAAGATGGACAGACAAACCAATTAAT 13346
QY 366 ----- 365
Db 13345 TGCTGAATGGGTAGGAATTAAGACATTAAGAAATTAAGGAAAGAACACAAAGATATTAA 13286
QY 366 ----- 365
Db 13285 AATGTTTTCATTAATTTTGTGCTCTCCCTGAATTTCTCCTGATTTCTCAGCCCAAT 13226
QY 366 ----- 365
Db 13225 CCCAAGCCAGGGTATCTCTGCTTTTACATCTCCCTCCACACTTTTGTGCTCATTA 13166
QY 366 ----- 365
Db 13165 TGTGCGGTGTGCTCACTTTCTTTGGTAGTTGCATATTCAATTAATCCCAACTTTCAAG 13106
QY 366 ----- 365
Db 13105 TCCGTGAAGGTGAGGATACAGAGAGGCTCATCTCCGATCCCTCAGCTCCCTTCTCTGA 13046
QY 366 ----- 365
Db 13045 AGCTGTACTAGTACAGTACCAAGTATGTTTCTTAAATGTAAGTAAATGATCATCAT 12986
QY 366 ----- 365
Db 12985 GAAAGAGCAATGTTTACCTTGACCAAAACACAGGCAAGGTGACTAGTGTGGTCAAG 12926
QY 366 ----- 365
Db 12925 AGATCCGTGCTGCTGGGAATCAGGAAAGGCTGCATGAGAAAGTGCAATTTTAGTTAGA 12866

QY 366 ----- 365
Db 12865 ACTTGAAAGTGTGTATTTAGTTTTCTGTGCTGCCATATTTCTTGTACATTGCTC 12806
QY 366 ----- 365
Db 12805 TCCATCTTCAGCCACTGGGCAAGGCTGAAAGCCCTCAGACATATCGGTAGGAATGT 12746
QY 366 ----- 365
Db 12745 GGAAGTTGAAGCTCAGAGTGCAGAAAGAAACAGTAGCATTTTAGAAAAAGCTAAATC 12686
QY 366 ----- 365
Db 12685 CCCCAAGAAATACCTCAATCATCGTAAAAAGCTGTAGTAGAGCACTAACACTCAAG 12626
QY 366 ----- 365
Db 12625 GCACTGCTTACAGAGTAAAGAACGTAAATGAAAACTGAGAAAGAGAAACTGTGT 12566
QY 366 ----- 365
Db 12565 CTGTACTGCAGAAAGCTTAGCAGATTTGTGTCTGTGATATATGGACACAGAGCTTG 12506
QY 366 ----- 365
Db 12505 TAAATGATGAATTTGAATGCTTATCCGAAAGGTTTCCAAATAAAATGTGAAAGCAAG 12446
QY 366 ----- 365
Db 12445 CCTGTTTCTTCTGCTCTTTATAGTAAATGCAAGAGAGAGAGAAATAGAGGAAAG 12386
QY 366 ----- 365
Db 12385 AACTTAAACAGAAAGAAACAGAGCTTGATGATTTGGAGGTTCTCAACTATGCAAAAA 12326
QY 366 ----- 365
Db 12325 ACNATAAATTAAGAGATTGAGTGGGCAAGTGGCTCATGCTGTATCCAGCACTT 12266
QY 366 ----- 365
Db 12265 TGAAGTCCAGGCGAGAGATCACTGAGGTCAAGATTGAGACAGCCTGGCCATG 12206
QY 366 ----- 365
Db 12205 TGGGAAACTCGGTCTTACTTAAAAATACAAAAATTAAGCTGGGTGTGGCGGCACTT 12146
QY 366 ----- 365
Db 12145 GTAATCCAGTACTCAGAGAGCTGAGGTGGAGAGATCACTTGAAACCAAGGCGGAG 12086
QY 366 ----- 365
Db 12085 TTGCAGTAGCCAGATATGCCACTGCACTCAGCCTGGGTGGGTGACAGAGCAAGACT 12026
QY 366 ----- 365
Db 12025 CCATCTCAAAAAAAAAAAAAAAAAAGAGTGTCTCCAAAAGTGTGACATAGAGAAACAGC 11966
QY 366 ----- 365
Db 11965 CAAATATGTATTAATACCAAACTTCAGAGAGATAAAGATCAAAAGTACTAGTGCCTCAA 11906
QY 366 ----- 365
Db 11905 AAAGCTTTGAAGAGATTAGATTATTAATCAACAGTCCCTTCAATCAAAACAGGGGAGC 11846
QY 366 ----- 365
Db 11845 TTCTAGAAAGCTGAACAGCATTTGCTCCTCAGCCATCTCAGCTGAGCCAAAAGTAGAGAA 11786

QY 366 ----- 365
Db 11785 GGGCTTATCGAAAAAGATGTGTGACCTGGCTTTATCTAATAATGACGTGATTC 11726
QY 366 ----- 365
Db 11725 CCCATGACATCCATAGGAGACCCGTAAGTTCTGAGACGTTTACATCCACAGAAACACT 11666
QY 366 ----- 365
Db 11665 GTTAGCTTGATTAATGGAACACAGAGATGATAATCAAGAAGGCTGTGGACTTC 11606
QY 366 ----- 365
Db 11605 CAGTTTCTACTGTGAGATGCAGCTGTAATACTACTAGTCGCAACACTGTACT 11546
QY 366 ----- 365
Db 11545 TTAGTGAAGAAGAGATATCTCAGACGATGAACAGAACTCAAGGCGAGTGAAG 11486
QY 366 ----- 365
Db 11485 AGCGAAAGAGATTCTCCAGGCTTGAAACCTAATGAGTTTCTTGGCTGATTTTC 11426
QY 366 ----- 365
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 Db 4885 ACCCTGCAAGAGCAAGAGAGAGAGATGAGAGAGACAGAGATGAGCTGACCTTC 4826
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 Db 4405 AGGAGAGAGAGAGGCGAGGAGATTAAGAAATTGAGAGACAGGATGCGGAGCACTGGAGG 4346
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 Db 4345 CTGAGAGCACCCAGAGAGCCGAGAGCAGAGGCGGAGCAATTGGGCAATTAATGCGCAGGT 4286
 QY 1475 GA 1476
 Db 4285 GA 4284

RESULT 2
 AL358412 17352 bp DNA linear HTG 30-OCT-2000
 LOCUS Home sapiens chromosome 1 clone RP11-509F14, *** SEQUENCING IN
 DEFINITION
 PROGRESSES ***, 16 unordered pieces.
 ACCESSION AL358412

VERSION AL358412.9 GI:11071692
 KEYWORDS HTG, HTGS_PHASE1.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 17352)
 Sins.8
 Direct Submission
 Submitted (29-OCT-2000) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk
 requests: clonerequests@sanger.ac.uk
 On Nov 1, 2000 this sequence version replaced gi:11071629.
 ----- Genome Center
 Center: Sanger Centre
 Center code: SC
 Web site: http://www.sanger.ac.uk
 Contact: humquerry@sanger.ac.uk
 ----- Project Information
 Center project name: BA509F14
 ----- Summary Statistics
 Assembly program: XGAP4, version 4.5
 Sequencing vector: plasmid; 108752; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Consensus quality: 167382 bases at least Q40
 Consensus quality: 169011 bases at least Q30
 Consensus quality: 170100 bases at least Q20
 Insert size: 171852; sum-of-contigs
 Insert size: 189168; agarose-fp
 Quality coverage: 5.54x in Q20 bases, sum-of-contigs Quality
 coverage: 5.15x in Q20 bases, agarose-fp

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 16 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 9825: contig of 9825 bp in length
 * 9826 9925: gap of 100 bp
 * 26226 26225: contig of 16300 bp in length
 * 26326 26325: gap of 100 bp
 * 26326 26317: contig of 3192 bp in length
 * 29518 29517: gap of 100 bp
 * 35633 35632: contig of 6015 bp in length
 * 35733 35732: gap of 100 bp
 * 49745 49744: contig of 1403 bp in length
 * 49846 49845: gap of 100 bp
 * 66204 66203: contig of 16359 bp in length
 * 66205 66204: gap of 100 bp
 * 72839 72838: contig of 6535 bp in length
 * 72940 72939: gap of 100 bp
 * 83723 83722: contig of 10783 bp in length
 * 83823 83822: gap of 100 bp
 * 91894 91893: contig of 8072 bp in length
 * 91895 91894: gap of 100 bp
 * 103783 103782: contig of 11789 bp in length
 * 103784 103783: gap of 100 bp
 * 110994 110993: contig of 7111 bp in length
 * 110995 110994: gap of 100 bp
 * 127550 127549: contig of 16456 bp in length
 * 127551 127550: gap of 100 bp
 * 137959 137958: contig of 10309 bp in length
 * 137960 137959: gap of 100 bp
 * 151496 151495: contig of 13437 bp in length
 * 151497 151496: gap of 100 bp
 * 154539 154538: contig of 2943 bp in length
 * 154540 154539: gap of 100 bp
 * 173352 173351: contig of 18713 bp in length.

FEATURES
 source

Location/Qualifiers
 1..173352